

Multipartite viruses: a decentralized mode of functioning

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Multipartite viruses are characterized by a genome composed of two or more nucleic acid segments, each encapsidated individually. A classical view in virology assumes that the viral replication cycle occurs within individual cells, where the whole viral genome information is replicated, and is then reiterated in successively infected cells during host invasion. In the context of multipartite viruses, this view implies that at least one copy of each of the genome segments must enter in each of the infected cells. The genome of the Faba bean necrotic stunt virus (FBNSV, Family *Nanoviridae*) is composed of 8 ssDNA circles of about 1000 bases, each encapsidated in an individual virus particle. We have previously shown that each of the eight segments reproducibly accumulates at a specific relative frequency, some representing around 30% of the total viral DNA within an infected plant and others not exceeding 2%. In this situation, it is difficult to conceive how FBNSV can actually transmit the whole genome information both from cell to cell and from host to host. If the segments enter cells indifferently, solely according to their frequency within the population, we could calculate that a successful infection of 95% of the susceptible cells would require the entry of nearly 200 particles per cell. This figure illustrates the enormous cost that FBNSV might bear at each cell-to-cell transmission step. Alternatively, this virus might infect individual cells with subgroups of genome segments, partial genome information being replicated at distinct location within a host. This may alleviate the cost at cell-to-cell passage but would imply a sort of unknown viral communication or complementation in between these subgroups of segments to maintain the integrity of the genome information. In any cases, the actual functioning of FBNSV is an enigma, because it is hard to conceive that a virus could force hundreds of particles in each newly colonized cells, or that the genome could function with separate subunits in distinct cells. We are currently developing tools to test the above alternatives.

Mots-clés : *Nanovirus, Faba bean necrotic stunt virus*, cell-autonomous replication, RNA/protein trafficking.